

SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences

City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use of a structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

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<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1).. (189)

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gaa	agc	gag	tgg	gtc	aag	gct	gga	gtg	cag	aaa	tat	ggg	gaa	gga	aac	96
Glu	Ser	Glu	Trp	Val	Lys	Ala	Gly	Val	Gln	Lys	Tyr	Gly	Glu	Gly	Asn	
		20					25						30			

tgg	gct	gcc	att	tct	aaa	aat	tac	cca	ttt	gtt	aac	cga	aca	gct	gtg	144
Trp	Ala	Ala	Ile	Ser	Lys	Asn	Tyr	Pro	Phe	Val	Asn	Arg	Thr	Ala	Val	
		35					40					45				

atg	att	aag	gat	cgc	tgg	cgg	acc	atg	aaa	aga	ctt	ggc	atg	aac	189
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn  
50 55 60

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
20 25 30  
tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144  
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val  
35 40 45  
atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189  
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val  
 35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn  
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 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
 20 25 30  
 tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144  
 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val  
 35 40 45  
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 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn  
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 35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn  
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
 20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144  
 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val  
 35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189  
 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn  
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
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 35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn  
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96  
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn  
 20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144  
 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val  
 35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac	189
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
50 55 60

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg	144
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Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val  
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac  
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn  
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189

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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn  
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48

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac  
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn

96

	20		25		30	
tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg						144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val						
	35		40		45	
atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac						189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn						
	50		55		60	

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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	

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35 40 45	

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn	
50 55 60	

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agg cgg gcg tcc cgc agt agc ggg cgg gcc cgg cgg ggg cgc cac gag	96
Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu	



20	25	30	
ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu 35 40 45			144
gaa gag gca gtc aat cgc tgg gtg ctc aag ttc tac ttc cac gag gcg Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala 50 55 60			192
ctg cgg gcc ttt cgg ggt agc cgg tac ggg gac ttc aga cag atc cgg Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg 65 70 75 80			240
gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr 85 90 95			288
gtg tcc cga ttg ctg cgg gtt atg cag tgt ctg tgc cgg att gaa gaa Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu 100 105 110			336
ggg gaa aat tta gac tgt tcc ttt gat atg gag gct gag ctc aca cca Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro 115 120 125			384
ctg gaa tca gct atc aat gtg ctg gag atg att aaa acg gaa ttt aca Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr 130 135 140			432
ctg aca gaa gca gtg gtc gaa tcc agt aga aaa ctg gtc aag gaa gct Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala 145 150 155 160			480
gct gtc att att tgt atc aaa aac aaa gaa ttt gaa aag gct tca aaa Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys 165 170 175			528
att ttg aaa aaa cat atg tcc aag gac ccc aca act cag aag ctg aga Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg 180 185 190			576
aat gat ctc ctg aat att att cga gaa aag aac ttg gcc cat cct gtt Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val 195 200 205			624
atc cag aac ttt tca tat gag acc ttc cag cag aag atg ctg cgc ttc Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe 210 215 220			672
ctg gag agc cac ctg gat gac gcc gag ccc tac ctc ctc acg atg gcc Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala 225 230 235 240			720

aaa aag gct ttg aaa tct gag tcc gct gcc tca agt aca ggg aag gaa	768
Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu	
245 250 255	
gat aaa cag cca gca cca ggg cct gtg gaa aag cca ccc aga gaa ccc	816
Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro	
260 265 270	
gca agg cag cta cgg aat cct cca acc acc att gga atg atg act ctg	864
Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu	
275 280 285	
aaa gca gct ttc aag act ctg tct ggt gca cag gat tct gag gca gcc	912
Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala	
290 295 300	
ttt gca aaa ctg gac cag aag gat ctg gtt ctt cct act caa gct ctc	960
Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu	
305 310 315 320	
cca gca tca cca gcc ctc aaa aac aag aga ccc aga aaa gat gaa aac	1008
Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn	
325 330 335	
gaa agt tca gcc ccg gct gac ggt gag ggt ggc tcg gaa ctg cag ccc	1056
Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro	
340 345 350	
aag aac aag cgc atg aca ata agc aga ttg gtc ttg gag gag gac agc	1104
Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser	
355 360 365	
cag agt act gag ccc agc gca ggc ctc aac tcc tcc cag gag gcc gct	1152
Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala	
370 375 380	
tca gcg cca cca tcc aag ccc acc gtt ctc aac caa ccc ctc cct gga	1200
Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly	
385 390 395 400	
gag aag aat ccc aaa gta ccc aaa ggc aag tgg aac agc tct aat ggg	1248
Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly	
405 410 415	
gtt gaa gaa aag gag act tgg gtg gaa gag gat gaa ctg ttt caa gtt	1296
Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val	
420 425 430	
cag gca gca cca gat gaa gac agt aca acc aat ata aca aaa aag cag	1344
Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln	
435 440 445	
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Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys	

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tat ggg gaa gga aac tgg gct gcc att tct aaa aat tac cca ttt gtt			1440
Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val			
465	470	475	480
aac cga aca gct gtg atg att aag gat cgc tgg cgg acc atg aaa aga			1488
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Leu Gly Met Asn			
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35 40 45

Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala  
50 55 60

Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg  
65 70 75 80

Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr  
85 90 95

Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu  
100 105 110

Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro  
115 120 125

Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr  
130 135 140

Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala  
145 150 155 160

Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys  
165 170 175

Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg  
180 185 190

Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val  
195 200 205

Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe  
210 215 220

Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala  
225 230 235 240

Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu  
245 250 255

Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro  
260 265 270

Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu  
275 280 285

Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala  
290 295 300

Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu  
305 310 315 320

Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn  
325 330 335

Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro  
340 345 350

Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser  
355 360 365

Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala  
370 375 380

Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly  
385 390 395 400

Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly  
405 410 415

Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val  
420 425 430

Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln  
435 440 445

Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys  
450 455 460

Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val  
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13

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13

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36

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27

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27

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aaccgaacat ctgtgatgat taaggat

27

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27

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37